



```
690 700 710 720 730 740 750
GGTACCGCGCGGCTTACAGGACACCTTTGGGGCGGTGAGGAACATCTACACCCCGGCGGAGTGGCCACCGAAT
760 770 780 790 800 810 820
CCGGAAGCTAGACCATCCAGAGCGGGGGCAATACGTGCTGGAGGCCAGGAGCCCTTCAAGAAACTCAA
830 840 850 860 870 880 890 900
GTGAGTCGGTCTCCCCACCGCCACCCACCATTTAGGTGCGCTATAGTGTGGGTTGATATGAAGAAATGCAGA
CAT
CAT
X
900 910 920 930 940 950 960
TCCCTACCCCCACACCT-CAGTGGTGGAGGCTGTGACTTCTC-GGTGATGTTGATGCCCTCAAAACT
|||||
ATGCTAACAGCATAAACATGAGGGGTG-GGACGAGG---TCACAAAGTGTGTTG---TCA--ATT
10 20 30 40 50 60
970 980 990 1000 1010 1020 1030
CTCGTTGAGTGGGGGTAGA---GGTTGACACTGTGACTGGAGA-----AGGAA-TTTCAC-TTGGGTCA
|||||
CTACTTGA-ATGAAGCTTGAATAATTAACAGT-ACGGGAATGCCAGGCAATTTCTCTCTGGTGA
70 80 90 100 110 120 130
1040 1050 1060 1070 1080 1090
GCAGTA-GGAGT-AA-ACTTAAATCTGTATATAACACAGCAATCTTAAGAAATAAAGGATCTCT
|||||
-CATATAGTCTCAACACTTGGAA-GTATTTTAAAGATGTTTAT-TTAAATTAAGAGTGGATTCCA
140 150 160 170 180 190 200
1100 1110 1120 1130 1140 1150 1160
TGAAGGTTAGTGACCAACTGATATTTGCGTCTTCTGTCAGTTTTTCTTCTTCTCTTA-TTTT
|||||
AGGAA-AAAATAGGAAGGAAGAAAGAAACTGAACAAACGCAAAAGTATACGTTGTCCTAAC
210 220 230 240 250 260 270
1180 1190 1200 1210 1220 1230 1240
TTTTCTTGGAAATCCATCTTTTAAATTA-ATAACATCTTAAATAATCA-CTTCCAGTGTGGACACT
|||||
CTTTCAGAGTACTTTTATTTCTTAAAGATCTGTTGTTTATACAGATTTTAAAGTTT---ACTC-
280 290 300 310 320 330 340
1250 1260 1270 1280 1290 1300
ATATTG-TCACAGAGGAGAAATGCTCTCAATTCCTG-ACTGTTTAAATTTCAACCTTTC-ATTC
|||||
CTACTGTCACC-CAAGTGA-AATTCCT-----TCTCCAGTCACAGTGA---ACCTCTACCCCAACTG
350 360 370 380 390 400
1310 1320 1330 1340 1350 1360 1370
CAAGTAGA--ATTGA-----CAACACTCACTTTTGTGA---CCCTGCTCC-CACCCCTGCATTTATGCTG
|||||
CAACGAGATTTGAGGGGCAATCAATCAC-ACCAGAGAGTCACAGCCCTCAACCACTG-AGGTGTTGGGGG
410 420 430 440 450 460 470
1380 X
TTAGCATATG
|||||
GTAGGATCTGCTTTCTATATCAACCCACACTATAGGGCACTTAATGGTGGCGGTGGGGAGACC
480 490 500 510 520 530 540
GACTCATTGAGTTTCTGAAGGCTTCTGTGCTCCAGCCACGTAATGGCCCGCTCTGATCTGCTAG
550 560 570 580 590 600 610 620
CTTCCGGATTCCGTTGGCGGCGGTGTAGATGTTCTGACGGCCCAAGAGGTGCTCAACCCCGCC
630 640 650 660 670 680 690
GGTCACTCTCTCAGGAAGACTTGAAGCTGGACACCTTCTTCTCATGATGACGCGCGCCCGCGTA
700 710 720 730 740 750 760
GAAGGGTCCCGTTGCGGTACACAGCACCTCTTCAACGACGGGTGAGACAGGTGGCTGGACCTGGCGCT
770 780 790 800 810 820 830
```

```
GTCCCGCTCATCTTCCCGCTGGCGCGCTCAGCTCGCTTCGCTCGGAGGACCTCCGCTGTC
840 850 860 870 880 890 900
CAGCGGCTCACCCACCCAGGCGCGGATCGCTCTCTGAACGAGAGAACTGACGATCCACAGGTG
910 920 930 940 950 960 970 980
AAAGAGA
```

3. US-09-674-593-1' (1-1382)  
US-09-674-593-10 Sequence 10, Application US/09674593

Sequence 10, Application US/09674593

GENERAL INFORMATION:

APPLICANT: Van den Eynde, Benoit

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND  
FILE REFERENCE: L0461/7099

CURRENT APPLICATION NUMBER: US/09/674,593

CURRENT FILING DATE: 2000-06-07

PRIOR APPLICATION NUMBER: PC7/US99/10424

PRIOR FILING DATE: 1999-05-13

PRIOR APPLICATION NUMBER: US-60/085,318

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Window Version 3.0

SEQ ID NO 10

LENGTH: 246

TYPE: DNA

ORGANISM: Homo sapiens

Initial Score	-	54	Optimized Score	-	107	Significance	-	-0.24
Residue Identity	-	51%	Matches	-	137	Mismatches	-	85
Gaps	-	-	Conservative Substitutions	-	-	-	-	0

```
TCCATGAGAAGAAGGTGCCAGCTTCGAGTTCCTCTGAGGAGGTGACCGGCGGTTCAGGCACCCCTTTG
720 730 740 750 760 770 780
GGGCGGTGAGGAACATCTACACCCCGGAGTGGCCCAATCCGGAAGTAGACAGATCCACAGCGGGG
790 800 810 820 830 840 850
GCAATTACGTGGTGGAGCGGAGGAGGCTTCAGAAACTCAAGTGAAGTCTCCCGCCACCGCCACCA
860 870 880 890 900 910 920
TTTAGGTGCCCCATAGTGTGGGGTTGATATGAAGAAATGCAGATCCCTTACCCCCACACCTCAGTGTGA
930 940 950 960 970 980 990 1000
GGGCTCTGACTTCTCGGTGTGATTGATGCCCTCAAAACTCTCGTTCAGTGGGGGTAGAGTTGACAC
1010 1020 1030 1040 1050 1060 1070
TGTGACTGGAGAAGAAATTTCTTGGTTCAGCAGTAGGAGTAAATCTTAAATCTGTGTATAAACAAGGA
1080 1090 1100 1110 1120 1130 1140
ATCTTAAGAAATAAAGATGATCTCTGCAAGGTAGTGACCAACTGATATCTTTGGCTTTCTGTTCA
|||||
GTCA
X
1150 1160 1170 1180 1190 1200 1210
GTTTTTTCTTCC---TTTTCTTATTTTCTTGGAAATCCATCTTAAATTAATAAATCAATCTT
|||||
--TTAACCTTTGCAAGTACCTT-TTATTTTC-TTAAAGT---TCCTGT-TTTTATACAGATT-TT
10 20 30 40 50 60
1220 1230 1240 1250 1260 1270
AAAATCACTTCCAGTGTGGAC--ACT-ATATT--GTCAAG--AGGAGAAATGCTCTGCTCATTTCC
|||||
A-AGTTTAC-TCCTACTGCTGACCAAGTGAATCTTCTCCAGTCAAGTGTCAA--CCTCTAC---CCC
70 80 90 100 110 120 130
```

```
900 910 920 930 940 950 960
TGCA--GATCCCTACCCGCCACACCTAGTGGTGGGGCTGTGACTTCCTCGGTGTGATTGATGCGCCCTC
|||||
TGCATNGCTTNGTGGCTCCCAATGNGCCGACGCTCA--GGAAGGAAGTTGTGTAAGGA--GNACCCNGTT
420 430 440 450 460 470 480

970 980 990 1000 1010 1020 1030
AAACCTCTGCTGCTGCTGGGGGTAGAGTTGACACTGTGACTGTGAGAGGAATTTCACTTGG-GTCAGCA
|||||
ANAGTTTATAAGC--CTGGATGGA-TGGTTNGCGAGT-AATG-----NGAATCTCTGGGANTTTCCA
490 500 510 520 530 540

1040 1050 1060 1070 1080 1090 1100
GTAGAGTAAGCTTAAATCTGTGTAATAACACAGGAATCTTAAAGAAATATAAAGGTATCTTGCAAG
|||||
CT--GA-TCCAGTCCATC-----TTTACCCAGTAGNATC-----TCTCTCCNCTCC---CTTAT
550 560 570 580 590 600

1110 1120 1130 1140 1150 1160 1170
GTAGTGACCAACTGATCTTTTGGTCTTCTGTGCTAGTCTTTTCTTCTTCTTTCTTTTCTTTTCTTTTCTTT
|||||
GTATTTGGGAA
610 X

1180 1190 1200 1210 1220 1230 1240 1250
GGAAATCCATCTTTTAAATTAATAAACATCTTAAATAACATCTTCAAGTGTGGACACTATATTGTCAC
1260 1270 1280 1290 1300 1310 1320
CAGAGGAGAAATTCCTGCAATTTCCCGTACTGTTTAAATATTATTCACCTTTCATTCCAAGTGAATGA
1330 1340 1350 1360 1370 1380
CAACACTACTTTTGTGACCTGCTCCACCCCTGCATGTTATGCTTGTAGCATAATG
```

#### 5. US-09-674-593-1' (1-1382)

US-09-674-593-9 Sequence 9, Application US/09674593

Sequence 9, Application US/09674593

GENERAL INFORMATION:

APPLICANT: Van den Eynde, Benoit

APPLICANT: Boon-Fallier, Thierry

TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND

FILE REFERENCE: OF A NEW UBIQUITOUSLY EXPRESSED GENE

CURRENT APPLICATION NUMBER: US/09/674,593

CURRENT FILING DATE: 2000-06-07

PRIOR APPLICATION NUMBER: PCT/US99/10424

PRIOR FILING DATE: 1999-05-13

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Window Version 3.0

SEQ ID NO 9

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

Initial Score = 25 Optimized Score = 25 Significance = -0.37

Residue Identity = 100% Matches = 25 Mismatches = 0

Gaps = 0 Conservative Substitutions = 0

CCAGAACTTAATTCCTTAATTTGGGAGGAGCAGGAGATTGAGGGGTAAAGGTGCAAGAGAGAGAAAG

80 90 100 X 110 120 130 140

AAAATATGGCTGTTTGAAGGGTAGCAGATATGATGTAAGAAATTTGGGTTTCCACATATTTGTGTG

|||||

TAGGCTGTTTGAAGGGTAGCACA

X 10 20 X

150 160 170 180 190 200 210

TGTGTGTGTGCGCTCTCTCTCTGCTCTACTAGGCGTGCTTTTGAAGGCCCGCGGTTCGCG

```
220 230 240 250 260 270 280
CTCCTGCTCAGAAAGCTGTCCAGTATTCTCCCGTAGCAGGTGACCTGTGTTGGTCCGCGCACTGCGGG
290 300 310 320 330 340 350 360
TCCTGATTGGCTGTGCACGCCACGGTGAATAAATTTAGCGTCTACTCCGAGTCTCTGCAAGCTCCTAGTCTCT
370 380 390 400 410 420 430
CCTCTGGGTGGAGCGCTAGGCGCAGCGCGTTACTTCTTTTCACTGTGGATTCTGTCAGTTCTCTGTTCTG
440 450 460 470 480 490 500
TTACAGGAGCGATCCCGCGCCCTGGGTGCGGTGAGCGCTGGGACAGCGAGGTGCTTCCGACCGCAAGC
510 520 530 540 550 560 570
AGCGAGCTGAGCGCGCGCCAGCGGGGAGATGAGCGGCAGCAGCGCCAGGTCCACCCACCTGTCTCAGCCC
580 590 600
GTCGTGAAGAGCGCTTTGTGTACCGC
```

#### 6. US-09-674-593-1' (1-1382)

US-09-674-593-6 Sequence 6, Application US/09674593

Sequence 6, Application US/09674593

GENERAL INFORMATION:

APPLICANT: Van den Eynde, Benoit

APPLICANT: Boon-Fallier, Thierry

TITLE OF INVENTION: TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND

FILE REFERENCE: OF A NEW UBIQUITOUSLY EXPRESSED GENE

CURRENT APPLICATION NUMBER: US/09/674,593

CURRENT FILING DATE: 2000-06-07

PRIOR APPLICATION NUMBER: PCT/US99/10424

PRIOR FILING DATE: 1999-05-13

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Window Version 3.0

SEQ ID NO 6

LENGTH: 18

TYPE: DNA

ORGANISM: Homo sapiens

Initial Score = 18 Optimized Score = 18 Significance = -0.40

Residue Identity = 100% Matches = 18 Mismatches = 0

Gaps = 0 Conservative Substitutions = 0

GCTCCTGCTCAGAAAGCTGTCCACCTTGATTCTGCCGTAGCAGGTGAACCTGGTGTGCGCGCACTGCGG

220 230 240 250 260 270 280

290 300 310 320 330 340 350

GTCCTGATTGCTGTGCACGCCACGGTGAATAAATTTAGCGTCTACTCCGAGTCTCTGCAAGCTCTAGTCTC

360 370 380 390 400 410 420 430

TCCTCTGGGTGGAGCGCTTAGCGCACGGCCGTTACTTCTTCACTCTGTGATTCTGTCGTTCTCTGTTCTG

440 450 460 470 480 490 500

TTTCAGGAGCGATCCCGCGCCCTGGGTGCGGTGAGCGCGTGGGACAGCGGAGGTGCTCCCGACGCGAAG

510 520 530 540 550 560 570

CAGCGAGCTGAGCGCGCGCCAGCGGGAAGATGAGCGGACGCGCAGCGGTCACGACCTGCTCTCAGCC

580 590 600 610 620 630 640

CGTCTGTAAGAGCGTGTGTGTACCGCAACGGGACCCCTTCTACGGGGCGCGCGTCTCTCATCCATGA

650 660 670 680 690 700 710 X

GAGAAGGTGTCCAGCTTCAAGTCTTCTCTGAAGGAGGTGACCGCGGCGGTTTCAGGACCCCTTTGGGGCGGT

|||||

CCGT X

720 730 X 740 750 760 770 780 790

CAGGAACATCTACACCCCGCGGACTGGCCACCGCAATCCGGAAGCTAGACCAGATCCAGAGCGGGGCAATTA

|||||

[illegible]

[illegible]

DB Z57 CCGCTGGCCGCCCGCTCAGCTCGCTCGCTTCGCTCGGAGGCACTCCGCTGTGTCACAGCG Z58

**D<sub>b</sub>**    GCCTACCGCACCCAGGCGGGATCGCCTCTGAACGAACTGCAGCAATCC 178

**QY**    974    acagggcgcgaaggaaacccgcccaccacacacaga  
||||| ||||| |

db 177 ACAGGTGAAGAGAGAAGTAACGGCCGTCGCCCTAGCGCTCCACCCAGAGGAGACACTAGGA 118

[illegible]

Uy 1034 gctctgcaggacccctcgggagctagagcgcctcaggctctctccacccgctggcgtccacagcgcacatcagg 1035

db 117 GCTTGCAGGACTCGGAGTAGACGCTCAAGTTTTTCACCGTGGCGTCACAGCCAATCAGG 58

0v 1094 accacagtagccgcacccacacacaggttcacctctctacgggcagaaatcacagctggac 1150

Db 57 ACCGGCAGTGGGGCCACACACCGAGGTTCACTGCTACGGGCAGAAATCAAGGTGGAC 1

## RESULT 2

US-09-674-393-4

Query Match . 2.28; Score 30; DB 1; Length 2167;

```

Best Local Similarity 49.4%;   Pred: NO: 0;
Matches 78: Conservative 0: Mismatches 80: Indels 0: Gaps

```

[illegible]

799 t t c a c g a c g g g c t a g a g a c a g g t a g c t a g c c t a g a c c t a g c c c t a t c t c c c c g c t 858

Db 315 agcgcaagtccagcacctgtctacgccgctcgtgaagagcgtgttctgtaccgcac 374  
QY 859 ggcgcgcgcctcagctcgtgtcttcgcgtcggaggca 896  
||| ||| ||| ||| ||| ||| ||| |||  
Db 375 gggaacctttacggggcgccgcgtcatcca 412

Job time: 3 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2002, 07:32:44 ; Search time 0.01 Seconds  
(without alignments)  
3.998 Million cell updates/sec

Title: us-09-674-593-2  
Perfect score: 451  
Sequence: 1 MDDAPRVGVAVHKHA.....GAGSPETNEKLTNPQVKE 84

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 476 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 2 summaries

Database: us-09-674-593-5.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	11.3	476	1	us-09-674-593-5

# ALIGNMENTS

RESULT 1  
us-09-674-593-5

Query Match 11.3%; Score 51; DB 1; Length 476;  
Best Local Similarity 23.1%; Pred. No. 0;  
Matches 21; Conservative 10; Mismatches 40; Indels 20; Gaps 2;  
(QY 4 DAAPRVGVAVHKHLDGLRVAGGAAAAHLPRWPPQOLAASRRAPFLSQRPHT 63  
DB 383 DAPEQVE-----EILDHSEQQARPARVNGTDEENGELQQVNNELQLVLDKERKS 433  
QY 64 QGAGS-----PPETNEKLTNPQVKE 83  
DB 434 QGAGSGQDEADVDPORPPRPVKITSPEENE 464

Search completed: September 6, 2002, 07:32:44  
Job time: 0 sec







